

SEQUENCE LISTING

<110> DNAVEC RESEARCH INC.

<120> Method of treating ischemic disease

<130> D3-A0208P

<150> JP 2003-040806

<151> 2003-02-19

<160> 9

<170> PatentIn version 3.1

<210> 1

<211> 3372

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(3372)

<223>

<400> 1

atg gac tct tta gcc agc tta gtt ctc tgt gga gtc agc ttg ctc ctt 48

Met Asp Ser Leu Ala Ser Leu Val Leu Cys Gly Val Ser Leu Leu Leu

1

5

10

15

tct gga act gtg gaa ggt gcc atg gac ttg atc ttg atc aat tcc cta 96

Ser Gly Thr Val Glu Gly Ala Met Asp Leu Ile Leu Ile Asn Ser Leu

20

25

30

cct ctt gta tct gat gct gaa aca tct ctc acc tgc att gcc tct ggg 144

Pro Leu Val Ser Asp Ala Glu Thr Ser Leu Thr Cys Ile Ala Ser Gly

35

40

45

tgg cgc ccc cat gag ccc atc acc ata gga agg gac ttt gaa gcc tta 192

Trp Arg Pro His Glu Pro Ile Thr Ile Gly Arg Asp Phe Glu Ala Leu

50	55	60	
atg aac cag cac cag gat ccg ctg gaa gtt act caa gat gtg acc aga			240
Met Asn Gln His Gln Asp Pro Leu Glu Val Thr Gln Asp Val Thr Arg			
65	70	75	80
gaa tgg gct aaa aaa gtt gtt tgg aag aga gaa aag gct agt aag atc			288
Glu Trp Ala Lys Lys Val Val Trp Lys Arg Glu Lys Ala Ser Lys Ile			
	85	90	95
aat ggt gct tat ttc tgt gaa ggg cga gtt cga gga gag gca atc agg			336
Asn Gly Ala Tyr Phe Cys Glu Gly Arg Val Arg Gly Glu Ala Ile Arg			
	100	105	110
ata cga acc atg aag atg cgt caa caa gct tcc ttc cta cca gct act			384
Ile Arg Thr Met Lys Met Arg Gln Gln Ala Ser Phe Leu Pro Ala Thr			
	115	120	125
tta act atg act gtg gac aag gga gat aac gtg aac ata tct ttc aaa			432
Leu Thr Met Thr Val Asp Lys Gly Asp Asn Val Asn Ile Ser Phe Lys			
	130	135	140
aag gta ttg att aaa gaa gaa gat gca gtg att tac aaa aat ggt tcc			480
Lys Val Leu Ile Lys Glu Glu Asp Ala Val Ile Tyr Lys Asn Gly Ser			
	145	150	155
			160
ttc atc cat tca gtg ccc cgg cat gaa gta cct gat att cta gaa gta			528
Phe Ile His Ser Val Pro Arg His Glu Val Pro Asp Ile Leu Glu Val			
	165	170	175
cac ctg cct cat gct cag ccc cag gat gct gga gtg tac tcg gcc agg			576
His Leu Pro His Ala Gln Pro Gln Asp Ala Gly Val Tyr Ser Ala Arg			
	180	185	190
tat ata gga gga aac ctc ttc acc tcg gcc ttc acc agg ctg ata gtc			624
Tyr Ile Gly Gly Asn Leu Phe Thr Ser Ala Phe Thr Arg Leu Ile Val			
	195	200	205
cgg aga tgt gaa gcc cag aag tgg gga cct gaa tgc aac cat ctc tgt			672
Arg Arg Cys Glu Ala Gln Lys Trp Gly Pro Glu Cys Asn His Leu Cys			

210	215	220	
act gct tgt atg aac aat ggt gtc tgc cat gaa gat act gga gaa tgc			720
Thr Ala Cys Met Asn Asn Gly Val Cys His Glu Asp Thr Gly Glu Cys			
225	230	235	240
att tgc cct cct ggg ttt atg gga agg acg tgt gag aag gct tgt gaa			768
Ile Cys Pro Pro Gly Phe Met Gly Arg Thr Cys Glu Lys Ala Cys Glu			
	245	250	255
ctg cac acg ttt ggc aga act tgt aaa gaa agg tgc agt gga caa gag			816
Leu His Thr Phe Gly Arg Thr Cys Lys Glu Arg Cys Ser Gly Gln Glu			
	260	265	270
gga tgc aag tct tat gtg ttc tgt ctc cct gac ccc tat ggg tgt tcc			864
Gly Cys Lys Ser Tyr Val Phe Cys Leu Pro Asp Pro Tyr Gly Cys Ser			
	275	280	285
tgt gcc aca ggc tgg aag ggt ctg cag tgc aat gaa gca tgc cac cct			912
Cys Ala Thr Gly Trp Lys Gly Leu Gln Cys Asn Glu Ala Cys His Pro			
	290	295	300
ggt ttt tac ggg cca gat tgt aag ctt agg tgc agc tgc aac aat ggg			960
Gly Phe Tyr Gly Pro Asp Cys Lys Leu Arg Cys Ser Cys Asn Asn Gly			
305	310	315	320
gag atg tgt gat cgc ttc caa gga tgt ctc tgc tct cca gga tgg cag			1008
Glu Met Cys Asp Arg Phe Gln Gly Cys Leu Cys Ser Pro Gly Trp Gln			
	325	330	335
ggg ctc cag tgt gag aga gaa ggc ata ccg agg atg acc cca aag ata			1056
Gly Leu Gln Cys Glu Arg Glu Gly Ile Pro Arg Met Thr Pro Lys Ile			
	340	345	350
gtg gat ttg cca gat cat ata gaa gta aac agt ggt aaa ttt aat ccc			1104
Val Asp Leu Pro Asp His Ile Glu Val Asn Ser Gly Lys Phe Asn Pro			
	355	360	365
att tgc aaa gct tct ggc tgg ccg cta cct act aat gaa gaa atg acc			1152
Ile Cys Lys Ala Ser Gly Trp Pro Leu Pro Thr Asn Glu Glu Met Thr			

370	375	380	
ctg gtg aag ccg gat ggg aca gtg ctc cat cca aaa gac ttt aac cat			1200
Leu Val Lys Pro Asp Gly Thr Val Leu His Pro Lys Asp Phe Asn His			
385	390	395	400
acg gat cat ttc tca gta gcc ata ttc acc atc cac cgg atc ctc ccc			1248
Thr Asp His Phe Ser Val Ala Ile Phe Thr Ile His Arg Ile Leu Pro			
	405	410	415
cct gac tca gga gtt tgg gtc tgc agt gtg aac aca gtg gct ggg atg			1296
Pro Asp Ser Gly Val Trp Val Cys Ser Val Asn Thr Val Ala Gly Met			
	420	425	430
gtg gaa aag ccc ttc aac att tct gtt aaa gtt ctt cca aag ccc ctg			1344
Val Glu Lys Pro Phe Asn Ile Ser Val Lys Val Leu Pro Lys Pro Leu			
	435	440	445
aat gcc cca aac gtg att gac act gga cat aac ttt gct gtc atc aac			1392
Asn Ala Pro Asn Val Ile Asp Thr Gly His Asn Phe Ala Val Ile Asn			
	450	455	460
atc agc tct gag cct tac ttt ggg gat gga cca atc aaa tcc aag aag			1440
Ile Ser Ser Glu Pro Tyr Phe Gly Asp Gly Pro Ile Lys Ser Lys Lys			
465	470	475	480
ctt cta tac aaa ccc gtt aat cac tat gag gct tgg caa cat att caa			1488
Leu Leu Tyr Lys Pro Val Asn His Tyr Glu Ala Trp Gln His Ile Gln			
	485	490	495
gtg aca aat gag att gtt aca ctc aac tat ttg gaa cct cgg aca gaa			1536
Val Thr Asn Glu Ile Val Thr Leu Asn Tyr Leu Glu Pro Arg Thr Glu			
	500	505	510
tat gaa ctc tgt gtg caa ctg gtc cgt cgt gga gag ggt ggg gaa ggg			1584
Tyr Glu Leu Cys Val Gln Leu Val Arg Arg Gly Glu Gly Gly Glu Gly			
	515	520	525
cat cct gga cct gtg aga cgc ttc aca aca gct tct atc gga ctc cct			1632
His Pro Gly Pro Val Arg Arg Phe Thr Thr Ala Ser Ile Gly Leu Pro			

530	535	540	
cct cca aga ggt cta aat ctc ctg cct aaa agt cag acc act cta aat			1680
Pro Pro Arg Gly Leu Asn Leu Leu Pro Lys Ser Gln Thr Thr Leu Asn			
545	550	555	560
ttg acc tgg caa cca ata ttt cca agc tcg gaa gat gac ttt tat gtt			1728
Leu Thr Trp Gln Pro Ile Phe Pro Ser Ser Glu Asp Asp Phe Tyr Val			
	565	570	575
gaa gtg gag aga agg tct gtg caa aaa agt gat cag cag aat att aaa			1776
Glu Val Glu Arg Arg Ser Val Gln Lys Ser Asp Gln Gln Asn Ile Lys			
	580	585	590
gtt cca ggc aac ttg act tcg gtg cta ctt aac aac tta cat ccc agg			1824
Val Pro Gly Asn Leu Thr Ser Val Leu Leu Asn Asn Leu His Pro Arg			
	595	600	605
gag cag tac gtg gtc cga gct aga gtc aac acc aag gcc cag ggg gaa			1872
Glu Gln Tyr Val Val Arg Ala Arg Val Asn Thr Lys Ala Gln Gly Glu			
	610	615	620
tgg agt gaa gat ctc act gct tgg acc ctt agt gac att ctt cct cct			1920
Trp Ser Glu Asp Leu Thr Ala Trp Thr Leu Ser Asp Ile Leu Pro Pro			
625	630	635	640
caa cca gaa aac atc aag att tcc aac att aca cac tcc tcg gct gtg			1968
Gln Pro Glu Asn Ile Lys Ile Ser Asn Ile Thr His Ser Ser Ala Val			
	645	650	655
att tct tgg aca ata ttg gat ggc tat tct att tct tct att act atc			2016
Ile Ser Trp Thr Ile Leu Asp Gly Tyr Ser Ile Ser Ser Ile Thr Ile			
	660	665	670
cgt tac aag gtt caa ggc aag aat gaa gac cag cac gtt gat gtg aag			2064
Arg Tyr Lys Val Gln Gly Lys Asn Glu Asp Gln His Val Asp Val Lys			
	675	680	685
ata aag aat gcc acc atc att cag tat cag ctc aag ggc cta gag cct			2112
Ile Lys Asn Ala Thr Ile Ile Gln Tyr Gln Leu Lys Gly Leu Glu Pro			

690	695	700	
gaa aca gca tac cag gtg gac att ttt gca gag aac aac ata ggg tca			2160
Glu Thr Ala Tyr Gln Val Asp Ile Phe Ala Glu Asn Asn Ile Gly Ser			
705	710	715	720
agc aac cca gcc ttt tct cat gaa ctg gtg acc ctc cca gaa tct caa			2208
Ser Asn Pro Ala Phe Ser His Glu Leu Val Thr Leu Pro Glu Ser Gln			
	725	730	735
gca cca gcg gac ctc gga ggg ggg aag atg ctg ctt ata gcc atc ctt			2256
Ala Pro Ala Asp Leu Gly Gly Gly Lys Met Leu Leu Ile Ala Ile Leu			
	740	745	750
ggc tct gct gga atg acc tgc ctg act gtg ctg ttg gcc ttt ctg atc			2304
Gly Ser Ala Gly Met Thr Cys Leu Thr Val Leu Leu Ala Phe Leu Ile			
	755	760	765
ata ttg caa ttg aag agg gca aat gtg caa agg aga atg gcc caa gcc			2352
Ile Leu Gln Leu Lys Arg Ala Asn Val Gln Arg Arg Met Ala Gln Ala			
	770	775	780
ttc caa aac gtg agg gaa gaa cca gct gtg cag ttc aac tca ggg act			2400
Phe Gln Asn Val Arg Glu Glu Pro Ala Val Gln Phe Asn Ser Gly Thr			
785	790	795	800
ctg gcc cta aac agg aag gtc aaa aac aac cca gat cct aca att tat			2448
Leu Ala Leu Asn Arg Lys Val Lys Asn Asn Pro Asp Pro Thr Ile Tyr			
	805	810	815
cca gtg ctt gac tgg aat gac atc aaa ttt caa gat gtg att ggg gag			2496
Pro Val Leu Asp Trp Asn Asp Ile Lys Phe Gln Asp Val Ile Gly Glu			
	820	825	830
ggc aat ttt ggc caa gtt ctt aag gcg cgc atc aag aag gat ggg tta			2544
Gly Asn Phe Gly Gln Val Leu Lys Ala Arg Ile Lys Lys Asp Gly Leu			
	835	840	845
cgg atg gat gct gcc atc aaa aga atg aaa gaa tat gcc tcc aaa gat			2592
Arg Met Asp Ala Ala Ile Lys Arg Met Lys Glu Tyr Ala Ser Lys Asp			

850	855	860	
gat cac agg gac ttt gca gga gaa ctg gaa gtt ctt tgt aaa ctt gga			2640
Asp His Arg Asp Phe Ala Gly Glu Leu Glu Val Leu Cys Lys Leu Gly			
865	870	875	880
cac cat cca aac atc atc aat ctc tta gga gca tgt gaa cat cga ggc			2688
His His Pro Asn Ile Ile Asn Leu Leu Gly Ala Cys Glu His Arg Gly			
	885	890	895
tac ttg tac ctg gcc att gag tac gcg ccc cat gga aac ctt ctg gac			2736
Tyr Leu Tyr Leu Ala Ile Glu Tyr Ala Pro His Gly Asn Leu Leu Asp			
	900	905	910
ttc ctt cgc aag agc cgt gtg ctg gag acg gac cca gca ttt gcc att			2784
Phe Leu Arg Lys Ser Arg Val Leu Glu Thr Asp Pro Ala Phe Ala Ile			
	915	920	925
gcc aat agc acc gcg tcc aca ctg tcc tcc cag cag ctc ctt cac ttc			2832
Ala Asn Ser Thr Ala Ser Thr Leu Ser Ser Gln Gln Leu Leu His Phe			
	930	935	940
gct gcc gac gtg gcc cgg ggc atg gac tac ttg agc caa aaa cag ttt			2880
Ala Ala Asp Val Ala Arg Gly Met Asp Tyr Leu Ser Gln Lys Gln Phe			
945	950	955	960
atc cac agg gat ctg gct gcc aga aac att tta gtt ggt gaa aac tat			2928
Ile His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Gly Glu Asn Tyr			
	965	970	975
gtg gca aaa ata gca gat ttt gga ttg tcc cga ggt caa gag gtg tac			2976
Val Ala Lys Ile Ala Asp Phe Gly Leu Ser Arg Gly Gln Glu Val Tyr			
	980	985	990
gtg aaa aag aca atg gga agg ctc cca gtg cgc tgg atg gcc atc gag			3024
Val Lys Lys Thr Met Gly Arg Leu Pro Val Arg Trp Met Ala Ile Glu			
	995	1000	1005
tca ctg aat tac agt gtg tac aca acc aac agt gat gta tgg tcc			3069
Ser Leu Asn Tyr Ser Val Tyr Thr Thr Asn Ser Asp Val Trp Ser			

1010	1015	1020	
tat ggt	gtg tta cta tgg gag	att gtt agc tta gga	ggc aca ccc 3114
Tyr Gly	Val Leu Leu Trp Glu	Ile Val Ser Leu Gly	Gly Thr Pro
1025	1030	1035	
tac tgc	ggg atg act tgt gca	gaa ctc tac gag aag	ctg ccc cag 3159
Tyr Cys	Gly Met Thr Cys Ala	Glu Leu Tyr Glu Lys	Leu Pro Gln
1040	1045	1050	
ggc tac	aga ctg gag aag ccc	ctg aac tgt gat gat	gag gtg tat 3204
Gly Tyr	Arg Leu Glu Lys Pro	Leu Asn Cys Asp Asp	Glu Val Tyr
1055	1060	1065	
gat cta	atg aga caa tgc tgg	cgg gag aag cct tat	gag agg cca 3249
Asp Leu	Met Arg Gln Cys Trp	Arg Glu Lys Pro Tyr	Glu Arg Pro
1070	1075	1080	
tca ttt	gcc cag ata ttg gtg	tcc tta aac aga atg	tta gag gag 3294
Ser Phe	Ala Gln Ile Leu Val	Ser Leu Asn Arg Met	Leu Glu Glu
1085	1090	1095	
cga aag	acc tac gtg aat acc	acg ctt tat gag aag	ttt act tat 3339
Arg Lys	Thr Tyr Val Asn Thr	Thr Leu Tyr Glu Lys	Phe Thr Tyr
1100	1105	1110	
gca gga	att gac tgt tct gct	gaa gaa gcg gcc	3372
Ala Gly	Ile Asp Cys Ser Ala	Glu Glu Ala Ala	
1115	1120		

<210> 2

<211> 1124

<212> PRT

<213> Homo sapiens

<400> 2

Met Asp Ser Leu Ala Ser Leu Val Leu Cys Gly Val Ser Leu Leu Leu

1

5

10

15

9/22

Ser Gly Thr Val Glu Gly Ala Met Asp Leu Ile Leu Ile Asn Ser Leu
20 25 30

Pro Leu Val Ser Asp Ala Glu Thr Ser Leu Thr Cys Ile Ala Ser Gly
35 40 45

Trp Arg Pro His Glu Pro Ile Thr Ile Gly Arg Asp Phe Glu Ala Leu
50 55 60

Met Asn Gln His Gln Asp Pro Leu Glu Val Thr Gln Asp Val Thr Arg
65 70 75 80

Glu Trp Ala Lys Lys Val Val Trp Lys Arg Glu Lys Ala Ser Lys Ile
85 90 95

Asn Gly Ala Tyr Phe Cys Glu Gly Arg Val Arg Gly Glu Ala Ile Arg
100 105 110

Ile Arg Thr Met Lys Met Arg Gln Gln Ala Ser Phe Leu Pro Ala Thr
115 120 125

Leu Thr Met Thr Val Asp Lys Gly Asp Asn Val Asn Ile Ser Phe Lys
130 135 140

Lys Val Leu Ile Lys Glu Glu Asp Ala Val Ile Tyr Lys Asn Gly Ser
145 150 155 160

Phe Ile His Ser Val Pro Arg His Glu Val Pro Asp Ile Leu Glu Val
165 170 175

His Leu Pro His Ala Gln Pro Gln Asp Ala Gly Val Tyr Ser Ala Arg
180 185 190

Tyr Ile Gly Gly Asn Leu Phe Thr Ser Ala Phe Thr Arg Leu Ile Val
195 200 205

Arg Arg Cys Glu Ala Gln Lys Trp Gly Pro Glu Cys Asn His Leu Cys
210 215 220

Thr Ala Cys Met Asn Asn Gly Val Cys His Glu Asp Thr Gly Glu Cys

225		230		235		240
Ile Cys Pro Pro Gly Phe Met Gly Arg Thr Cys Glu Lys Ala Cys Glu						
	245		250		255	
Leu His Thr Phe Gly Arg Thr Cys Lys Glu Arg Cys Ser Gly Gln Glu						
	260		265		270	
Gly Cys Lys Ser Tyr Val Phe Cys Leu Pro Asp Pro Tyr Gly Cys Ser						
	275		280		285	
Cys Ala Thr Gly Trp Lys Gly Leu Gln Cys Asn Glu Ala Cys His Pro						
	290		295		300	
Gly Phe Tyr Gly Pro Asp Cys Lys Leu Arg Cys Ser Cys Asn Asn Gly						
305		310		315		320
Glu Met Cys Asp Arg Phe Gln Gly Cys Leu Cys Ser Pro Gly Trp Gln						
	325		330		335	
Gly Leu Gln Cys Glu Arg Glu Gly Ile Pro Arg Met Thr Pro Lys Ile						
	340		345		350	
Val Asp Leu Pro Asp His Ile Glu Val Asn Ser Gly Lys Phe Asn Pro						
	355		360		365	
Ile Cys Lys Ala Ser Gly Trp Pro Leu Pro Thr Asn Glu Glu Met Thr						
	370		375		380	
Leu Val Lys Pro Asp Gly Thr Val Leu His Pro Lys Asp Phe Asn His						
385		390		395		400
Thr Asp His Phe Ser Val Ala Ile Phe Thr Ile His Arg Ile Leu Pro						
	405		410		415	
Pro Asp Ser Gly Val Trp Val Cys Ser Val Asn Thr Val Ala Gly Met						
	420		425		430	
Val Glu Lys Pro Phe Asn Ile Ser Val Lys Val Leu Pro Lys Pro Leu						
	435		440		445	

Asn Ala Pro Asn Val Ile Asp Thr Gly His Asn Phe Ala Val Ile Asn
 450 455 460

Ile Ser Ser Glu Pro Tyr Phe Gly Asp Gly Pro Ile Lys Ser Lys Lys
 465 470 475 480

Leu Leu Tyr Lys Pro Val Asn His Tyr Glu Ala Trp Gln His Ile Gln
 485 490 495

Val Thr Asn Glu Ile Val Thr Leu Asn Tyr Leu Glu Pro Arg Thr Glu
 500 505 510

Tyr Glu Leu Cys Val Gln Leu Val Arg Arg Gly Glu Gly Gly Glu Gly
 515 520 525

His Pro Gly Pro Val Arg Arg Phe Thr Thr Ala Ser Ile Gly Leu Pro
 530 535 540

Pro Pro Arg Gly Leu Asn Leu Leu Pro Lys Ser Gln Thr Thr Leu Asn
 545 550 555 560

Leu Thr Trp Gln Pro Ile Phe Pro Ser Ser Glu Asp Asp Phe Tyr Val
 565 570 575

Glu Val Glu Arg Arg Ser Val Gln Lys Ser Asp Gln Gln Asn Ile Lys
 580 585 590

Val Pro Gly Asn Leu Thr Ser Val Leu Leu Asn Asn Leu His Pro Arg
 595 600 605

Glu Gln Tyr Val Val Arg Ala Arg Val Asn Thr Lys Ala Gln Gly Glu
 610 615 620

Trp Ser Glu Asp Leu Thr Ala Trp Thr Leu Ser Asp Ile Leu Pro Pro
 625 630 635 640

Gln Pro Glu Asn Ile Lys Ile Ser Asn Ile Thr His Ser Ser Ala Val
 645 650 655

Ile Ser Trp Thr Ile Leu Asp Gly Tyr Ser Ile Ser Ser Ile Thr Ile		
660	665	670
Arg Tyr Lys Val Gln Gly Lys Asn Glu Asp Gln His Val Asp Val Lys		
675	680	685
Ile Lys Asn Ala Thr Ile Ile Gln Tyr Gln Leu Lys Gly Leu Glu Pro		
690	695	700
Glu Thr Ala Tyr Gln Val Asp Ile Phe Ala Glu Asn Asn Ile Gly Ser		
705	710	715 720
Ser Asn Pro Ala Phe Ser His Glu Leu Val Thr Leu Pro Glu Ser Gln		
725	730	735
Ala Pro Ala Asp Leu Gly Gly Gly Lys Met Leu Leu Ile Ala Ile Leu		
740	745	750
Gly Ser Ala Gly Met Thr Cys Leu Thr Val Leu Leu Ala Phe Leu Ile		
755	760	765
Ile Leu Gln Leu Lys Arg Ala Asn Val Gln Arg Arg Met Ala Gln Ala		
770	775	780
Phe Gln Asn Val Arg Glu Glu Pro Ala Val Gln Phe Asn Ser Gly Thr		
785	790	795 800
Leu Ala Leu Asn Arg Lys Val Lys Asn Asn Pro Asp Pro Thr Ile Tyr		
805	810	815
Pro Val Leu Asp Trp Asn Asp Ile Lys Phe Gln Asp Val Ile Gly Glu		
820	825	830
Gly Asn Phe Gly Gln Val Leu Lys Ala Arg Ile Lys Lys Asp Gly Leu		
835	840	845
Arg Met Asp Ala Ala Ile Lys Arg Met Lys Glu Tyr Ala Ser Lys Asp		
850	855	860
Asp His Arg Asp Phe Ala Gly Glu Leu Glu Val Leu Cys Lys Leu Gly		

865		870		875		880
His His Pro Asn Ile Ile Asn Leu Leu Gly Ala Cys Glu His Arg Gly						
		885		890		895
Tyr Leu Tyr Leu Ala Ile Glu Tyr Ala Pro His Gly Asn Leu Leu Asp						
		900		905		910
Phe Leu Arg Lys Ser Arg Val Leu Glu Thr Asp Pro Ala Phe Ala Ile						
		915		920		925
Ala Asn Ser Thr Ala Ser Thr Leu Ser Ser Gln Gln Leu Leu His Phe						
		930		935		940
Ala Ala Asp Val Ala Arg Gly Met Asp Tyr Leu Ser Gln Lys Gln Phe						
		945		950		955
				960		
Ile His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Gly Glu Asn Tyr						
		965		970		975
Val Ala Lys Ile Ala Asp Phe Gly Leu Ser Arg Gly Gln Glu Val Tyr						
		980		985		990
Val Lys Lys Thr Met Gly Arg Leu Pro Val Arg Trp Met Ala Ile Glu						
		995		1000		1005
Ser Leu Asn Tyr Ser Val Tyr Thr Thr Asn Ser Asp Val Trp Ser						
		1010		1015		1020
Tyr Gly Val Leu Leu Trp Glu Ile Val Ser Leu Gly Gly Thr Pro						
		1025		1030		1035
Tyr Cys Gly Met Thr Cys Ala Glu Leu Tyr Glu Lys Leu Pro Gln						
		1040		1045		1050
Gly Tyr Arg Leu Glu Lys Pro Leu Asn Cys Asp Asp Glu Val Tyr						
		1055		1060		1065
Asp Leu Met Arg Gln Cys Trp Arg Glu Lys Pro Tyr Glu Arg Pro						
		1070		1075		1080

Ser Phe Ala Gln Ile Leu Val Ser Leu Asn Arg Met Leu Glu Glu
 1085 1090 1095

Arg Lys Thr Tyr Val Asn Thr Thr Leu Tyr Glu Lys Phe Thr Tyr
 1100 1105 1110

Ala Gly Ile Asp Cys Ser Ala Glu Glu Ala Ala
 1115 1120

<210> 3

<211> 1494

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1494)

<223>

<400> 3

atg aca gtt ttc ctt tcc ttt gct ttc ctc gct gcc att ctg act cac 48
 Met Thr Val Phe Leu Ser Phe Ala Phe Leu Ala Ala Ile Leu Thr His
 1 5 10 15

ata ggg tgc agc aat cag cgc cga agt cca gaa aac agt ggg aga aga 96
 Ile Gly Cys Ser Asn Gln Arg Arg Ser Pro Glu Asn Ser Gly Arg Arg
 20 25 30

tat aac cgg att caa cat ggg caa tgt gcc tac act ttc att ctt cca 144
 Tyr Asn Arg Ile Gln His Gly Gln Cys Ala Tyr Thr Phe Ile Leu Pro
 35 40 45

gaa cac gat ggc aac tgt cgt gag agt acg aca gac cag tac aac aca 192
 Glu His Asp Gly Asn Cys Arg Glu Ser Thr Thr Asp Gln Tyr Asn Thr
 50 55 60

aac gct ctg cag aga gat gct cca cac gtg gaa ccg gat ttc tct tcc 240
 Asn Ala Leu Gln Arg Asp Ala Pro His Val Glu Pro Asp Phe Ser Ser

65	70	75	80	
cag aaa ctt caa cat ctg gaa cat gtg atg gaa aat tat act cag tgg				288
Gln Lys Leu Gln His Leu Glu His Val Met Glu Asn Tyr Thr Gln Trp				
	85	90	95	
ctg caa aaa ctt gag aat tac att gtg gaa aac atg aag tcg gag atg				336
Leu Gln Lys Leu Glu Asn Tyr Ile Val Glu Asn Met Lys Ser Glu Met				
	100	105	110	
gcc cag ata cag cag aat gca gtt cag aac cac acg gct acc atg ctg				384
Ala Gln Ile Gln Gln Asn Ala Val Gln Asn His Thr Ala Thr Met Leu				
	115	120	125	
gag ata gga acc agc ctc ctc tct cag act gca gag cag acc aga aag				432
Glu Ile Gly Thr Ser Leu Leu Ser Gln Thr Ala Glu Gln Thr Arg Lys				
	130	135	140	
ctg aca gat gtt gag acc cag gta cta aat caa act tct cga ctt gag				480
Leu Thr Asp Val Glu Thr Gln Val Leu Asn Gln Thr Ser Arg Leu Glu				
145	150	155	160	
ata cag ctg ctg gag aat tca tta tcc acc tac aag cta gag aag caa				528
Ile Gln Leu Leu Glu Asn Ser Leu Ser Thr Tyr Lys Leu Glu Lys Gln				
	165	170	175	
ctt ctt caa cag aca aat gaa atc ttg aag atc cat gaa aaa aac agt				576
Leu Leu Gln Gln Thr Asn Glu Ile Leu Lys Ile His Glu Lys Asn Ser				
	180	185	190	
tta tta gaa cat aaa atc tta gaa atg gaa gga aaa cac aag gaa gag				624
Leu Leu Glu His Lys Ile Leu Glu Met Glu Gly Lys His Lys Glu Glu				
	195	200	205	
ttg gac acc tta aag gaa gag aaa gag aac ctt caa ggc ttg gtt act				672
Leu Asp Thr Leu Lys Glu Glu Lys Glu Asn Leu Gln Gly Leu Val Thr				
	210	215	220	
cgt caa aca tat ata atc cag gag ctg gaa aag caa tta aac aga gct				720
Arg Gln Thr Tyr Ile Ile Gln Glu Leu Glu Lys Gln Leu Asn Arg Ala				

225	230	235	240	
acc acc aac aac agt gtc ctt cag aag cag caa ctg gag ctg atg gac				768
Thr Thr Asn Asn Ser Val Leu Gln Lys Gln Gln Leu Glu Leu Met Asp				
	245	250	255	
aca gtc cac aac ctt gtc aat ctt tgc act aaa gaa ggt gtt tta cta				816
Thr Val His Asn Leu Val Asn Leu Cys Thr Lys Glu Gly Val Leu Leu				
	260	265	270	
aag gga gga aaa aga gag gaa gag aaa cca ttt aga gac tgt gca gat				864
Lys Gly Gly Lys Arg Glu Glu Glu Lys Pro Phe Arg Asp Cys Ala Asp				
	275	280	285	
gta tat caa gct ggt ttt aat aaa agt gga atc tac act att tat att				912
Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly Ile Tyr Thr Ile Tyr Ile				
	290	295	300	
aat aat atg cca gaa ccc aaa aag gtg ttt tgc aat atg gat gtc aat				960
Asn Asn Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val Asn				
305	310	315	320	
ggg gga ggt tgg act gta ata caa cat cgt gaa gat gga agt cta gat				1008
Gly Gly Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly Ser Leu Asp				
	325	330	335	
ttc caa aga ggc tgg aag gaa tat aaa atg ggt ttt gga aat ccc tcc				1056
Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro Ser				
	340	345	350	
ggt gaa tat tgg ctg ggg aat gag ttt att ttt gcc att acc agt cag				1104
Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln				
	355	360	365	
agg cag tac atg cta aga att gag tta atg gac tgg gaa ggg aac cga				1152
Arg Gln Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg				
	370	375	380	
gcc tat tca cag tat gac aga ttc cac ata gga aat gaa aag caa aac				1200
Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn				

385	390	395	400	
tat agg ttg tat tta aaa ggt cac act ggg aca gca gga aaa cag agc				1248
Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser				
	405	410	415	
agc ctg atc tta cac ggt gct gat ttc agc act aaa gat gct gat aat				1296
Ser Leu Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn				
	420	425	430	
gac aac tgt atg tgc aaa tgt gcc ctc atg tta aca gga gga tgg tgg				1344
Asp Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp				
	435	440	445	
ttt gat gct tgt ggc ccc tcc aat cta aat gga atg ttc tat act gcg				1392
Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala				
	450	455	460	
gga caa aac cat gga aaa ctg aat ggg ata aag tgg cac tac ttc aaa				1440
Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys				
	465	470	475	480
ggg ccc agt tac tcc tta cgt tcc aca act atg atg att cga cct tta				1488
Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr Met Met Ile Arg Pro Leu				
	485	490	495	
gat ttt				1494
Asp Phe				

<210> 4

<211> 498

<212> PRT

<213> Homo sapiens

<400> 4

Met Thr Val Phe Leu Ser Phe Ala Phe Leu Ala Ala Ile Leu Thr His

1

5

10

15

Ile Gly Cys Ser Asn Gln Arg Arg Ser Pro Glu Asn Ser Gly Arg Arg
 20 25 30

Tyr Asn Arg Ile Gln His Gly Gln Cys Ala Tyr Thr Phe Ile Leu Pro
 35 40 45

Glu His Asp Gly Asn Cys Arg Glu Ser Thr Thr Asp Gln Tyr Asn Thr
 50 55 60

Asn Ala Leu Gln Arg Asp Ala Pro His Val Glu Pro Asp Phe Ser Ser
 65 70 75 80

Gln Lys Leu Gln His Leu Glu His Val Met Glu Asn Tyr Thr Gln Trp
 85 90 95

Leu Gln Lys Leu Glu Asn Tyr Ile Val Glu Asn Met Lys Ser Glu Met
 100 105 110

Ala Gln Ile Gln Gln Asn Ala Val Gln Asn His Thr Ala Thr Met Leu
 115 120 125

Glu Ile Gly Thr Ser Leu Leu Ser Gln Thr Ala Glu Gln Thr Arg Lys
 130 135 140

Leu Thr Asp Val Glu Thr Gln Val Leu Asn Gln Thr Ser Arg Leu Glu
 145 150 155 160

Ile Gln Leu Leu Glu Asn Ser Leu Ser Thr Tyr Lys Leu Glu Lys Gln
 165 170 175

Leu Leu Gln Gln Thr Asn Glu Ile Leu Lys Ile His Glu Lys Asn Ser
 180 185 190

Leu Leu Glu His Lys Ile Leu Glu Met Glu Gly Lys His Lys Glu Glu
 195 200 205

Leu Asp Thr Leu Lys Glu Glu Lys Glu Asn Leu Gln Gly Leu Val Thr
 210 215 220

Arg Gln Thr Tyr Ile Ile Gln Glu Leu Glu Lys Gln Leu Asn Arg Ala

225		230		235		240
Thr Thr Asn Asn Ser Val Leu Gln Lys Gln Gln Leu Glu Leu Met Asp						
		245		250		255
Thr Val His Asn Leu Val Asn Leu Cys Thr Lys Glu Gly Val Leu Leu						
		260		265		270
Lys Gly Gly Lys Arg Glu Glu Glu Lys Pro Phe Arg Asp Cys Ala Asp						
		275		280		285
Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly Ile Tyr Thr Ile Tyr Ile						
		290		295		300
Asn Asn Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val Asn						
305		310		315		320
Gly Gly Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly Ser Leu Asp						
		325		330		335
Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro Ser						
		340		345		350
Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln						
		355		360		365
Arg Gln Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg						
		370		375		380
Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn						
385		390		395		400
Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser						
		405		410		415
Ser Leu Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn						
		420		425		430
Asp Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp						
		435		440		445

Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala
 450 455 460

Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys
 465 470 475 480

Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr Met Met Ile Arg Pro Leu
 485 490 495

Asp Phe

<210> 5

<211> 1744

<212> DNA

<213> Artificial

<220>

<223> artificially synthesized sequence

<400> 5

actagttatt aatagtaatc aattacgggg tcattagttc atagcccata tatggagttc	60
cgcgttacat aacttacggt aaatggcccc cctggctgac cgcccaacga ccccgccca	120
ttgacgtcaa taatgacgta tgttcccata gtaacgcaa tagggacttt ccattgacgt	180
caatgggtgg agtattttacg gtaaaactgcc cacttggcag tacatcaagt gtatcatatg	240
ccaagtacgc cccctattga cgtcaatgac ggtaaattggc ccgcctggca ttatgccag	300
tacatgacct tatgggactt tcctacttgg cagtacatct acgtattagt catcgctatt	360
accatggtcg aggtgagccc cacgttctgc ttactctcc ccatctcccc cccctcccca	420
cccccaattt tgtattttatt tattttttta ttattttgtg cagcgatggg ggcggggggg	480
gggggggggg gcgcgccagg cggggcgggg cggggcgagg ggcggggcgg ggcgaggcgg	540
agaggtgcgg cggcagccaa tcagagcggc gcgctccgaa agtttccttt tatggcgagg	600
cggcgggcgg ggcggcccta taaaaagcga agcgcgcggc gggcggggag tcgctgcgac	660
gctgccttcg ccccggtgcc cgctccgccc ccgcctcgcg ccgcccggcc cggctctgac	720
tgaccgcgtt actcccacag gtgagcgggc gggacggccc ttctcctccg ggctgtaatt	780
agcgcttggt ttaatgacgg cttgtttctt ttctgtggct gcgtgaaagc cttgaggggc	840
tccgggaggg ccctttgtgc ggggggagcg gctcgggggg tgctgtcgctg tgtgtgtgcg	900
tggggagcgc cgcgtgcggc tccgcgctgc ccggcggctg tgagcgtgc gggcgcggcg	960
cggggctttg tgcgctccgc agtgtgcgcg aggggagcgc ggccgggggc ggtgccccgc	1020

```

ggtgcggggg gggctgcgag gggaacaaag gctgcgtgcg ggggtgtgtgc gtgggggggt 1080
gagcaggggg tgtgggcgcg tcggtcgggc tgcaaccccc cctgcacccc cctccccgag 1140
ttgctgagca cggcccggct tcgggtgcgg ggctccgtac ggggcgtggc gcggggctcg 1200
ccgtgccggg cgggggggtgg cggcaggtgg gggtgccggg cggggcgggg ccgcctcggg 1260
ccggggaggg ctccggggag gggcgcggcg gcccccgag cggcggcggc tgtcgaggcg 1320
cggcgagccg cagccattgc cttttatggt aatcgtgcga gagggcgag ggacttcctt 1380
tgtcccaaat ctgtgcggag ccgaaatctg ggaggcgccg ccgcaccccc tctagcgggc 1440
gcggggcgaa gcggtgcggc gccggcagga aggaaatggg cggggagggc cttcgtgcgt 1500
cgccgcgcgc ccgtcccctt ctccctctcc agcctcgggg ctgtccgcgg ggggacggct 1560
gccttcgggg gggacggggc agggcggggt tcggcttctg gcgtgtgacc ggcggctcta 1620
gagcctctgc taacctgtt catgccttct tcttttctt acagctcctg ggcaacgtgc 1680
tggttattgt gctgtctcat ctttttgca aagaattcgg cttgatcgaa gcttgccac 1740
catg 1744

```

<210> 6
 <211> 30
 <212> DNA
 <213> Artificial

<220>
 <223> an artificially synthesized primer

```

<400> 6
cagaggcagt acatgctaag aattgagtta 30

```

<210> 7
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <223> an artificially synthesized primer

```

<400> 7
agatgctcaa ggggcttcat gatg 24

```

<210> 8

<211> 20

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer

<400> 8

tattgggcgc ctggcacca

20

<210> 9

<211> 20

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer

<400> 9

ccaccttctt gatgcatca

20